UNIVERSITY OF MINNESOTA
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Algorithm for Discovering Genetic Interactions in Genome-Wide Association Studies (BridGE)

IP Status: Pending Foreign Patent; **Application #:** 3017736

Bridging Gene Sets with Epistasis

BridGE (Bridging Gene Sets with Epistasis) is an innovative computational method that explicitly searches for disease-specific genetic interactions between single nucleotide polymorphisms (SNPs) in Genome-wide Association Studies (GWAS) data. The algorithm searches for larger, non-random structures of SNP-SNP interactions, guided by established sets of genes belonging to characterized pathways or gene modules. The concept was derived from extensive analysis of genetic interaction networks in yeast, which showed that genetic interactions tend to cluster between functionally compensatory pathways. If several SNPs interact between genes coding for proteins/pathways with redundant functions, the likelihood of obtaining statistical significance by searching for larger clusters of SNP-SNP interactions is much greater than if individual SNP interactions were considered separately. Applying BridGE broadly, significant interactions were discovered in Parkinson's disease, schizophrenia, hypertension, prostate cancer, type 2 diabetes and breast cancer.

Maps Complex Genetic Networks Underlying Human Disease

Detecting genetic interactions is important for fully characterizing heritability of complex diseases within Genome Wide Association Studies (GWAS). Current methods for detecting such genetic interactions are inaccurate, lacking statistical power and failing to reliably detect genetic interactions important for characterizing the heritability of complex diseases. By explicitly searching GWAS data for disease-specific genetic interactions between pathways, BridGE identifies large, non-random clusters that tend to contain genetic interactions. The technology has the potential to transform interpretation of human genome data and expand the therapeutic target space for complex genetic diseases.

BENEFITS AND FEATURES:

- Analyzes GWAS, whole genome sequencing (WGS), and whole exome sequencing (WES) data
- Identifies large, non-random clusters that contain genetic interactions
- Likely more reliable than existing detection of genetic interactions
- Identifies genetic interactions (SNPs) between genes within specific signaling pathways
- May help understand genetic risk or protective factors for particular diseases
- May help understand effectiveness of therapeutic strategies (e.g. pharmacological agents) in treating various conditions
- Additional features as needed

APPLICATIONS:

Technology ID
20160109

Category
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Life Sciences/Biomarkers
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Publications

Discovering genetic interactions bridging pathways in genome-wide association studies
bioRxiv, August 30, 2017
Pathway-based discovery of genetic interactions in breast cancer
PLOS Genetics, Sept 28, 2017